



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Susan DYMECKI
- (ii) TITLE OF INVENTION: Use of Flp Recombinase in Mice
- (iii) NUMBER OF SEQUENCES: 23
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
- (B) STREET: 1100 New York Avenue, N.W.
- (C) CITY: Washington
- (D) STATE: D.C.
- (E) COUNTRY: USA
- (F) ZIP: 20005-3918

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: Microsoft Word

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/866,279
- (B) FILING DATE: 30-MAY-1997
- (C) CLASSIFICATION:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCGGTGAAGT TCCTATTCG AAGTTCCTAT TCTCTAGAAA GTATAGGAAC 50

TTCCTTAGGA GATCTTCGAA GGCTCGAGC 79

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TAGCTACGTA GAAGTTCCTA TTCCGAAGTT CCTATTCTCT AGAAAGTATA 50
GGAAGTTCA 59

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTAGGGAAGT TCCTATACTT TCTAGAGAAT AGGAACTTCG GAATAGGAAC 50
TTCA 54

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CCGGTGAAGT TCCTATACTT TCTAGAGAAT AGGAACTTCG GAATAGGAAC 50
TTCTACGTAG CTAGCTCGAG CCTTCGAAGA TCTC 84

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTAAGGTACC GGTGAAGTTC CTA

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(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTCACCCACC GGTGAAGTTC CTA

23

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 211 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGTACCGAGC TCAGCCACCA TGACTGCTCC AAAGAAGAAG CGTAAGGTAC

50

CGGTGAAGTT CCTATTCCGA AGTTCCTATT CTCTAGAAAG TATAGGAACT

100

TCACCGGTGG GTGAAGACCA GAAACAGCAC CTCGAACCTGA GCCGCGATAT

150

TGCCACGCGT TTCAACGCGC TGTATGGCGA GATCGATCCC GTCGTTTTAC

200

AACGTCGTGA C

211

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Thr Ala Pro Lys Lys Lys Arg Lys Val Pro Val Lys Phe Leu
1 5 10 15
Phe Arg Ser Ser Tyr Ser Leu Glu Ser Ile Gly Thr Ser Pro Val
20 25 30
Gly Glu Asp Gln Lys Gln His Leu Glu Leu Ser Arg Asp Ile Ala
35 40 45
Gln Arg Phe Asn Ala Leu Tyr Gly Glu Ile Asp Pro Val Val Leu
50 55 60
Gln Arg Arg Asp

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Ala Pro Lys Lys Lys Arg Lys Val
1 5

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Lys Phe Leu Phe Arg Ser Ser Tyr Ser Leu Glu Ser Ile Gly Thr
1 5 10 15
Ser

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Pro Val Gly Glu Asp Gln Lys Gln His Leu Glu Leu Ser Arg Asp
1 5 10 15
Ile Ala Gln Arg Phe Asn Ala Leu Tyr Gly Glu Ile
20 25

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GAAGTTCCTA TTC 13

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAAGTTCCTA TAC 13

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GAAGTTCCTA TTCTCTAGAA AGTATAGGAA CTTC

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(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GAAGTTCCTA TTCCGAAGTT CCTATTCTCT AGAAAGTATA GGAAGTTC

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(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1272 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ATGCCACAAT TTGATATATT ATGTAAACA CCACCTAAGG TGCTTGTTG TCAGTTTGTG 60
 GAAAGGTTT AAGACCTTC AGGTGAGAAA ATAGCATTAT GTGCTGCTGA ACTAACCTAT 120
 TTATGTTGGA TGATTACACA TAACGGAACA GCAATCAAGA GAGCCACATT CATGAGCTAT 180
 AATACTATCA TAAGCAATTC GCTGAGTTG GATATTGTCA ACAAGTCACT GCAGTTTAAA 240
 TACAAGACGC AAAAAGCAAC AATTCTGGAA GCCTCATTA AGAATTGAT TCCTGCTTGG 300
 GAATTTACAA TTATTCCTTA CTATGGACA AAACATCAAT CTGATATCAC TGATATTGTA 360
 AGTAGTTTGC AATTACAGTT CGAATCATCG GAAGAAGCAG ATAAGGGAAA TAGCCACAGT 420
 AAAAAATGC TTAAGCACT TCTAAGTGAG GGTGAAAGCA TCTGGGAGAT CACTGAGAAA 480
 ATACTAAATT CGTTTGAGTA TACTTCGAGA TTTACAAAA CAAAACTTT ATACCAATTC 540
 CTCTTCCTAG CTACTTTCAT CAATTGTGGA AGATTCAGCG ATATTAAGAA CGTTGATCCG 600

AAATCATTTA AATTAGTCCA AAATAAGTAT CTGGGAGTAA TAATCCAGTG TTTAGTGACA 660
 GAGACAAAGA CAAGCGTTAG TAGGCACATA TACTTCTTTA GCGCAAGGGG TAGGATCGAT 720
 CCACTTGTAT ATTTGGATGA ATTTTGGAGG AATTCTGAAC CAGTCCTAAA ACGAGTAAAT 780
 AGGACCGGCA ATTCCTCAAG CAACAAGCAG GAATACCAAT TATTAAGA TAACCTAGTC 840
 AGATCGTACA ACAAAGCTTT GAAGAAAAAT GCGCCTTATT CAATCTTTGC TATAAAAAAT 900
 GGCCCAAAAT CTCACATTGG AAGACATTGG ATGACCTCAT TTCTTTCAAT GAAGGGCCTA 960
 ACGGAGTTGA CTAATGTTGT GGGAAATTGG AGCGATAAGC GTGCTTCTGC CGTGGCCAGG 1020
 ACAACGTATA CTCATCAGAT AACAGCAATA CCTGATCACT ACTTCGCACT AGTTTCTCGG 1080
 TACTATGCAT ATGATCCAAT ATCAAAGGAA ATGATAGCAT TGAAGGATGA GACTAATCCA 1140
 ATTGAGGAGT GGCAGCATAT AGAACAGCTA AAGGGTAGTG CTGAAGGAAG CATACGATAC 1200
 CCGCATGGA ATGGGATAAT ATCACAGGAG GTACTAGACT ACCTTTCATC CTACATAAAT 1260
 AGACGCATAT AA 1272

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met	Pro	Gln	Phe	Asp	Ile	Leu	Cys	Lys	Thr	Pro	Pro	Lys	Val	Leu
1				5					10					15
Val	Arg	Gln	Phe	Val	Glu	Arg	Phe	Glu	Arg	Pro	Ser	Gly	Glu	Lys
				20					25					30
Ile	Ala	Leu	Cys	Ala	Ala	Glu	Leu	Thr	Tyr	Leu	Cys	Trp	Met	Ile
				35					40					45
Thr	His	Asn	Gly	Thr	Ala	Ile	Lys	Arg	Ala	Thr	Phe	Met	Ser	Tyr
				50					55					60
Asn	Thr	Ile	Ile	Ser	Asn	Ser	Leu	Ser	Leu	Asp	Ile	Val	Asn	Lys
				65					70					75
Ser	Leu	Gln	Phe	Lys	Tyr	Lys	Thr	Gln	Lys	Ala	Thr	Ile	Leu	Glu
				80					85					90
Ala	Ser	Leu	Lys	Lys	Leu	Ile	Pro	Ala	Trp	Glu	Phe	Thr	Ile	Ile
				95					100					105
Pro	Tyr	Tyr	Gly	Gln	Lys	His	Gln	Ser	Asp	Ile	Thr	Asp	Ile	Val
				110					115					120

Ser Ser Leu Gln Leu Gln Phe Glu Ser Ser Glu Glu Ala Asp Lys
 125 130 135
 Gly Asn Ser His Ser Lys Lys Met Leu Lys Ala Leu Leu Ser Glu
 140 145 150
 Gly Glu Ser Ile Trp Glu Ile Thr Glu Lys Ile Leu Asn Ser Phe
 155 160 165
 Glu Tyr Thr Ser Arg Phe Thr Lys Thr Lys Thr Leu Tyr Gln Phe
 170 175 180
 Leu Phe Leu Ala Thr Phe Ile Asn Cys Gly Arg Phe Ser Asp Ile
 185 190 195
 Lys Asn Val Asp Pro Lys Ser Phe Lys Leu Val Gln Asn Lys Tyr
 200 205 210
 Leu Gly Val Ile Ile Gln Cys Leu Val Thr Glu Thr Lys Thr Ser
 215 220 225
 Val Ser Arg His Ile Tyr Phe Phe Ser Ala Arg Gly Arg Ile Asp
 230 235 240
 Pro Leu Val Tyr Leu Asp Glu Phe Leu Arg Asn Ser Glu Pro Val
 245 250 255
 Leu Lys Arg Val Asn Arg Thr Gln Asn Ser Ser Ser Asn Lys Gln
 260 265 270
 Glu Tyr Gln Leu Leu Lys Asp Asn Leu Val Arg Ser Tyr Asn Lys
 275 280 285
 Ala Leu Lys Lys Asn Ala Pro Tyr Ser Ile Phe Ala Ile Lys Asn
 290 295 300
 Gly Pro Lys Ser His Ile Gly Arg His Leu Met Thr Ser Phe Leu
 305 310 315
 Ser Met Lys Gly Leu Thr Glu Leu Thr Asn Val Val Gly Asn Trp
 320 325 330
 Ser Asp Lys Arg Ala Ser Ala Val Ala Arg Thr Thr Tyr Thr His
 335 340 345
 Gln Ile Thr Ala Ile Pro Asp His Tyr Phe Ala Leu Val Ser Arg
 350 355 360
 Tyr Tyr Ala Tyr Asp Pro Ile Ser Lys Glu Met Ile Ala Leu Lys
 365 370 375
 Asp Glu Thr Asn Pro Ile Glu Glu Trp Gln His Ile Glu Gln Leu
 380 385 390
 Lys Gly Ser Ala Glu Gly Ser Ile Arg Tyr Pro Ala Trp Asn Gly
 395 400 405
 Ile Ile Ser Gln Glu Val Leu Asp Tyr Leu Ser Ser Tyr Ile Asn
 410 415 420
 Arg Arg Ile

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1272 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

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ATGCCACAAT TTGATATATT ATGTAAAACA CCACCTAAGG TGCTTGTTGCG TCAGTTTGTG	60
GAAAGGTTTG AAAGACCTTC AGGTGAGAAA ATAGCATTAT GTGCTGCTGA ACTAACCTAT	120
TTATGTTGGA TGATTACACA TAACGGAACA GCAATCAAGA GAGCCACATT CATGAGCTAT	180
AATACTATCA TAAGCAATTC GCTGAGTTTC GATATTGTCA ACAAGTCACT GCAGTTTAAA	240
TACAAGACGC AAAAAGCAAC AATTCTGGAA GCCTCATTAAG AAAAATTGAT TCCTGCTTGG	300
GAATTTACAA TTATTCCTTA CTATGGACAA AACATCAAT CTGATATCAC TGATATTGTA	360
AGTAGTTTGC AATTACAGTT CGAATCATCG GAAGAAGCAG ATAAGGGAAA TAGCCACAGT	420
AAAAAATGCT TTAAGCACT TCTAAGTGAG GGTGAAAGCA TCTGGGAGAT CACTGAGAAA	480
ATACTAAATT CGTTTGAGTA TACTTCGAGA TTTACAAAA CAAAACTTT ATACCAATTC	540
CTCTTCCTAG CTACTTTCAT CAATTGTGGA AGATTCAGCG ATATTAAGAA CGTGTATCCG	600
AAATCATTTA AATTAGTCCA AAATAAGTAT CTGGGAGTAA TAATCCAGTG TTTAGTGACA	660
GAGACAAAGA CAAGCGTTAG TAGGCACATA TACTTCTTTA GCGCAAGGGG TAGGATCGAT	720
CCACTTGAT ATTTGGATGA ATTTTGGAGG AATTCTGAAC CAGTCTCTAA ACGAGTAAAT	780
AGGACCGGCA ATTCTTCAAG CAACAAGCAG GAATACCAAT TATTAAGA TAACITAGTC	840
AGATCGTACA ACAAGCTTT GAAGAAAAAT GCGCCTTATT CAATCTTTGC TATAAAAAAT	900
GGCCCAAAAT CTCACATTGG AAGACATTG ATGACCTCAT TTCTTTCAT GAAGGGCCTA	960
ACGGAGTTGA CTAATGTTGT GGGAAATTGG AGCGATAAGC GTGCTTCTGC CGTGCCAGG	1020
ACAACGTATA CTCATCAGAT AACAGCAATA CCTGATCACT ACTTCGCACT AGTTTCTCGG	1080
TACTATGCAT ATGATCCAAT ATCAAAGGAA ATGATAGCAT TGAAGGATGA GACTAATCCA	1140
ATTGAGGAGT GGCAGCATAT AGAACAGCTA AAGGGTAGTG CTGAAGGAAG CATACGATAC	1200
CCCGCATGGA ATGGGATAAT ATCACAGGAG GTACTAGACT ACCTTTCATC CTACATAAAT	1260
AGACGCATAT AA	1272

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 423 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Pro Gln Phe Asp Ile Leu Cys Lys Thr Pro Pro Lys Val Leu
1 5 10 15
Val Arg Gln Phe Val Glu Arg Phe Glu Arg Pro Ser Gly Glu Lys
20 25 30
Ile Ala Leu Cys Ala Ala Glu Leu Thr Tyr Leu Cys Trp Met Ile
35 40 45
Thr His Asn Gly Thr Ala Ile Lys Arg Ala Thr Phe Met Ser Tyr
50 55 60
Asn Thr Ile Ile Ser Asn Ser Leu Ser Phe Asp Ile Val Asn Lys
65 70 75
Ser Leu Gln Phe Lys Tyr Lys Thr Gln Lys Ala Thr Ile Leu Glu
80 85 90
Ala Ser Leu Lys Lys Leu Ile Pro Ala Trp Glu Phe Thr Ile Ile
95 100 105
Pro Tyr Tyr Gly Gln Lys His Gln Ser Asn Ile Thr Asp Ile Val
110 115 120
Ser Ser Leu Gln Leu Gln Phe Glu Ser Ser Glu Glu Ala Asp Lys
125 130 135
Gly Asn Ser His Ser Lys Lys Met Leu Lys Ala Leu Leu Ser Glu
140 145 150
Gly Glu Ser Ile Trp Glu Ile Thr Glu Lys Ile Leu Asn Ser Phe
155 160 165
Glu Tyr Thr Ser Arg Phe Thr Lys Thr Lys Thr Leu Tyr Gln Phe
170 175 180
Leu Phe Leu Ala Thr Phe Ile Asn Cys Gly Arg Phe Ser Asp Ile
185 190 195
Lys Asn Val Asp Pro Lys Ser Phe Lys Leu Val Gln Asn Lys Tyr
200 205 210
Leu Gly Val Ile Ile Gln Cys Leu Val Thr Glu Thr Lys Thr Ser
215 220 225
Val Ser Arg His Ile Tyr Phe Phe Ser Ala Arg Gly Arg Ile Asp
230 235 240
Pro Leu Val Tyr Leu Asp Glu Phe Leu Arg Asn Ser Glu Pro Val
245 250 255

Leu Lys Arg Val Asn Arg Thr Gln Asn Ser Ser Ser Asn Lys Gln
 260 265 270
 Glu Tyr Gln Leu Leu Lys Asp Asn Leu Val Arg Ser Tyr Asn Lys
 275 280 285
 Ala Leu Lys Lys Asn Ala Pro Tyr Ser Ile Phe Ala Ile Lys Asn
 290 295 300
 Gly Pro Lys Ser His Ile Gly Arg His Leu Met Thr Ser Phe Leu
 305 310 315
 Ser Met Lys Gly Leu Thr Glu Leu Thr Asn Val Val Gly Asn Trp
 320 325 330
 Ser Asp Lys Arg Ala Ser Ala Val Ala Arg Thr Thr Tyr Thr His
 335 340 345
 Gln Ile Thr Ala Ile Pro Asp His Tyr Phe Ala Leu Val Ser Arg
 350 355 360
 Tyr Tyr Ala Tyr Asp Pro Ile Ser Lys Glu Met Ile Ala Leu Lys
 365 370 375
 Asp Glu Thr Asn Pro Ile Glu Glu Trp Gln His Ile Glu Gln Leu
 380 385 390
 Lys Gly Ser Ala Glu Gly Ser Ile Arg Tyr Pro Ala Trp Asn Gly
 395 400 405
 Ile Ile Ser Gln Glu Val Leu Asp Tyr Leu Ser Ser Tyr Ile Asn
 410 415 420
 Arg Arg Ile

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGTCCAACTG CAGCCCAAGC TTCC

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(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:
GTGGATCGAT CCTACCCCTT GCG 23

(2) INFORMATION FOR SEQ ID NO:22:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:
GACTGCTCCA AAGAAGAAGC GTAAGG 26

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(2) INFORMATION FOR SEQ ID NO:23:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:
GCTATTACGC CAGCTGGCGA AAGG 24
